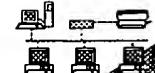


Devi

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/870,962

Art Unit / Team No. : 164/

Date Processed by STIC: 4/3/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

INPUT SET: S24665.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

3 (1) General Information

(i) APPLICANT: Duft, Bradford
Kolterman, Orville

(ii) TITLE OF THE INVENTION: METHODS FOR TREATING OBESITY

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: LYON & LYON
- (B) STREET: 633 WEST FIFTH STREET, SUITE 4700
- (C) CITY: LOS ANGELES
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/870,762
(B) FILING DATE: 06-JUN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: DUFT, BRADFORD J
(B) REGISTRATION NUMBER: 32,219
(C) REFERENCE/DOCKET NUMBER: 226/104

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 619-552-8400
- (B) TELEFAX: 619-552-0159
- (C) TELEX:

Does Not Comply
Corrected Diskette Needed

P.4

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762DATE: 04/03/98
TIME: 14:40:10

INPUT SET: S24665.raw

47 (2) INFORMATION FOR SEQ ID NO:1:
48
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 37 amino acids
51 (B) TYPE: amino acid
52 (C) STRANDEDNESS: single
53 (D) TOPOLOGY: linear
54
55 (ii) MOLECULE TYPE: peptide
56
57 (ix) FEATURE:
58 (B) LOCATION: 2,7
59 (D) OTHER INFORMATION: disulfide bridge between
60 the Cys residues
61 (B) LOCATION: 37
62 (D) OTHER INFORMATION: amidated Tyr
63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66
67 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
68 1 5 10 15
69 Leu Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr
70 20 25 30
71 Asn Val Gly Ser Asn Thr Tyr
72 35
73
74 (2) INFORMATION FOR SEQ ID NO:2:
75
76 (i) SEQUENCE CHARACTERISTICS:
77 (A) LENGTH: 37 amino acids
78 (B) TYPE: amino acid
79 (C) STRANDEDNESS: single
80 (D) TOPOLOGY: linear
81
82 (ii) MOLECULE TYPE: peptide
83
84 (ix) FEATURE:
85 (B) LOCATION: 2,7
86 (D) OTHER INFORMATION: disulfide bridge between
87 the Cys residues
88 (B) LOCATION: 37
89 (D) OTHER INFORMATION: amidated Tyr
90
91
92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
93
94 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
95 1 5 10 15
96 Leu Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr
97 20 25 30
98 Asn Val Gly Ser Asn Thr Tyr
99 35

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762DATE: 04/03/98
TIME: 14:40:11

INPUT SET: S24665.raw

100
101
102
103 (2) INFORMATION FOR SEQ ID NO:3:
104
105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 37 amino acids
107 (B) TYPE: amino acid
108 (C) STRANDEDNESS: single
109 (D) TOPOLOGY: linear
110
111 (ii) MOLECULE TYPE: Peptide
112
113 (ix) FEATURE:
114 (B) LOCATION: 2,7
115 (D) OTHER INFORMATION: disulfide bridge between
116 the Cys residues
117 (B) LOCATION: 37
118 (D) OTHER INFORMATION: amidated Tyr
119
120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
121
122 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
123 1 5 10 15
124 Leu Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr
125 20 25 30
126 Asn Val Gly Ser Asn Thr Tyr
127 35
128
129 (2) INFORMATION FOR SEQ ID NO:4:
130
131 (i) SEQUENCE CHARACTERISTICS:
132 (A) LENGTH: 37 amino acids
133 (B) TYPE: amino acid
134 (C) STRANDEDNESS: single
135 (D) TOPOLOGY: linear
136
137 (ii) MOLECULE TYPE: Peptide
138
139 (ix) FEATURE:
140 (B) LOCATION: 2,7
141 (D) OTHER INFORMATION: disulfide bridge between
142 the Cys residues
143 (B) LOCATION: 37
144 (D) OTHER INFORMATION: amidated Tyr
145
146 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
147
148 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
149 1 5 10 15
150 Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Pro Ser Thr
151 20 25 30
152 Asn Val Gly Ser Asn Thr Tyr

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762DATE: 04/03/98
TIME: 14:40:12

INPUT SET: S24665.raw

153

35

154

(2) INFORMATION FOR SEQ ID NO:5:

155

156

157

(i) SEQUENCE CHARACTERISTICS:

158

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

161

162

(ii) MOLECULE TYPE: peptide

163

164

(ix) FEATURE:

165

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between the Cys residues

166

167

(B) LOCATION: 37

168

- (D) OTHER INFORMATION: amidated Tyr

169

170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

171

172

173

Lys	Cys	Asn	Thr	Ala	Thr	Cys	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1						5			10				15	

174

Leu	Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Pro	Val	Leu	Pro	Pro	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

175

176

20

25

30

177

Asn	Val	Gly	Ser	Asn	Thr	Tyr
-----	-----	-----	-----	-----	-----	-----

178

35

179

180

181

182

(2) INFORMATION FOR SEQ ID NO:6:

183

184

(i) SEQUENCE CHARACTERISTICS:

185

186

187

188

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

189

190

(ii) MOLECULE TYPE: peptide

191

(ix) FEATURE:

192

193

194

195

- (B) LOCATION: 2,7
- (D) OTHER INFORMATION: disulfide bridge between the Cys residues

196

197

- (B) LOCATION: 37
- (D) OTHER INFORMATION: amidated Tyr

198

199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

200

201

Lys	(Asp)	Asn	Thr	Ala	Thr	(Lys)	Ala	Thr	Gln	Arg	Leu	Ala	Asn	Phe
1						5			10				15	

202

203

Leu	Val	His	Ser	Ser	Asn	Asn	Phe	Gly	Ala	Ile	Leu	Ser	Ser	Thr
						20			25				30	

204

205

Asn	Val	Gly	Ser	Asn	Thr	Tyr
-----	-----	-----	-----	-----	-----	-----

"Cys" is not shown in location 2 or 7

Please edit
any subsequent
sequences showing
this error)

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762DATE: 04/03/98
TIME: 14:40:14

INPUT SET: S24665.raw

206 35
207
208
209 (2) INFORMATION FOR SEQ ID NO:7:
210
211 (i) SEQUENCE CHARACTERISTICS:
212 (A) LENGTH: 37 amino acids
213 (B) TYPE: amino acid
214 (C) STRANDEDNESS: single
215 (D) TOPOLOGY: linear
216
217 (ii) MOLECULE TYPE: peptide
218
219 (ix) FEATURE:
220 (B) LOCATION: 2,7
221 (D) OTHER INFORMATION: disulfide bridge between
222 the Cys residues
223 (B) LOCATION: 37
224 (D) OTHER INFORMATION: amidated Tyr
225
226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
227
228 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
229 1 5 10 15
230 Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr
231 20 25 30
232 Asn Val Gly Ser Asn Thr Tyr
233 35
234
235 (2) INFORMATION FOR SEQ ID NO:8:
236
237 (i) SEQUENCE CHARACTERISTICS:
238 (A) LENGTH: 37 amino acids
239 (B) TYPE: amino acid
240 (C) STRANDEDNESS: single
241 (D) TOPOLOGY: linear
242
243 (ii) MOLECULE TYPE: peptide
244
245 (ix) FEATURE:
246 (B) LOCATION: 2,7
247 (D) OTHER INFORMATION: disulfide bridge between
248 the Cys residues
249 (B) LOCATION: 37
250 (D) OTHER INFORMATION: amidated Tyr
251
252
253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
254
255 Ala Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
256 1 5 10 15
257 Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr
258 20 25 30

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/870,762

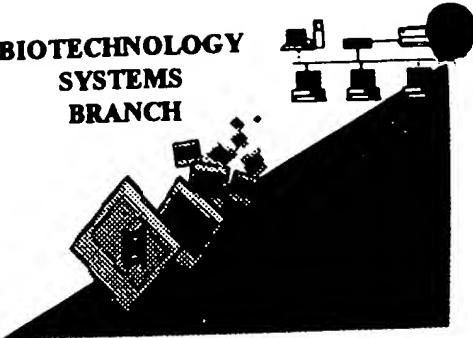
DATE: 04/03/98
TIME: 14:40:15

INPUT SET: S24665.raw

Line

Error

Original Text



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CRF 1.821 through 1.825). Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: pub/checker/
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
WASHINGTON DC 20231

COST FOR DISKETTE IS \$ 25.00

METHOD OF PAYMENT:

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PTO Deposit Account

For Further Information, Contact: Arti Shah at 703-308-4212